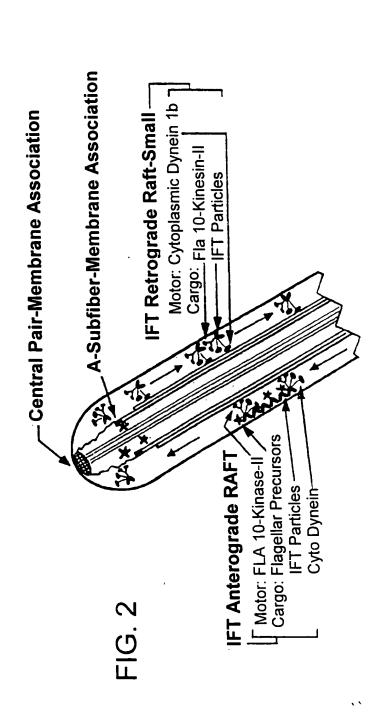


1.



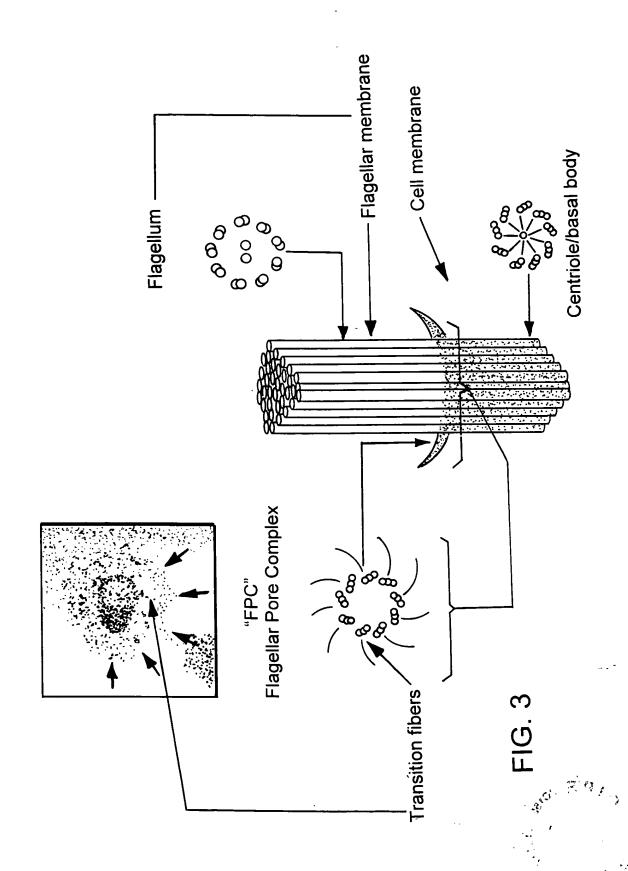
Out = Pre-assembled axonemal proteins In ** (radial spokes, dynein arms)
Synthesized on free polysomes

👃 = Heterotrimeric Kinesin II

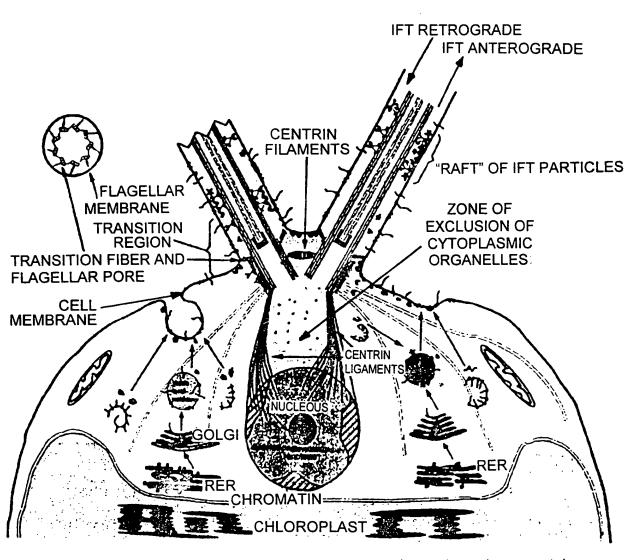
= IFT particle

= Cytoplamic Dynein 1b

4



4. Zj-



Y = IFT particle

= Heterotrimeric Kinesin II

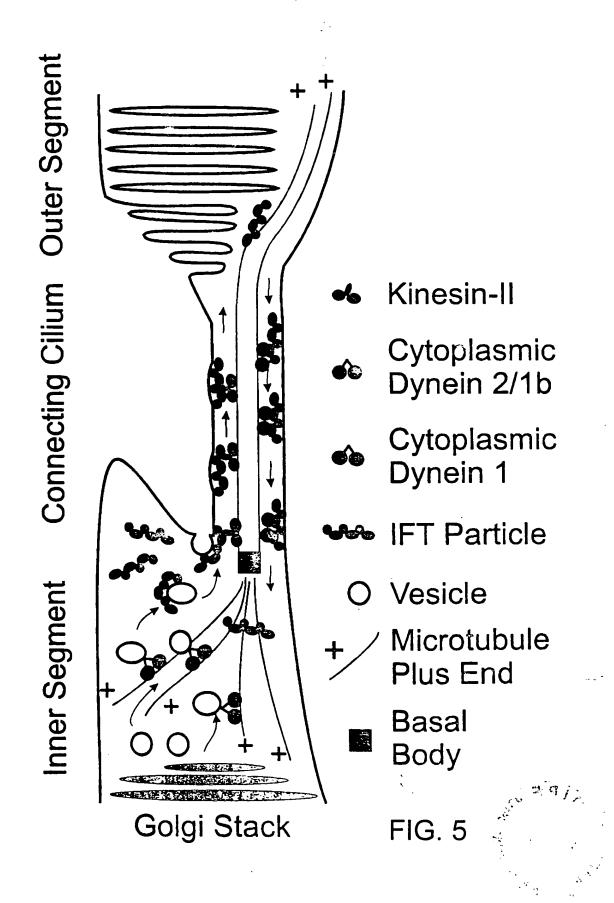
= Cytoplamic Dynein 1b

= Free Polysomes

= Microtubules

= Penpneral membrane (protein (ER—<mark>→</mark> Golgi) *™ 🤻*

FIG. 4



Chlamydomonas

>Cr_IFT20 predicted peptide
MDAVDRGVYFDEDFHVRILDVDKYNASKSLQDNTNVFINNIQNMQGLVDKYVSAIDQQVERLEA
EKLKAIGLRNRVAALSEERKRKQKEQERMLAEKQEELERLQMEEQSLIKVKGEQELMIQKLSDSS
SGAAYV (SEO ID NO: 2)

FIG. 6A

>Cr IFT20 cDNA CACCGCTGCCGCAGACAGTCTGCCAAAAC CAGCAGGCCTAGAGGTTGCCTTAACCTAAATATACAAAACACAGAGCATCATGGACGCGGTA GATAGAGGAGTCTACTTTGACGAGGACTTTCATGTCCGCATTCTTGATGTTGACAAGTACAAT GCTTCAAAGTCGCTCCAGGACAACACAAATGTGTTCATTAACAACATCCAAAATATGCAAGGC CTCGTGGACAAGTACGTGTCCGCCATCGACCAGCAGGTCGAGCGGCTAGAAGCTGAAAAGCT GAAGGCCATTGGCCTGCGGAACCGGGTGGCTGCGCTGAGCGAGGAGCGGAAACGTAAACAA AAGGAGCAGGAGCATGCTAGCGGAGAAGCAGGAGGAGCTTGAGAGGCTCCAAATGGAGG AGCAGTCGCTGATCAAGGTGAAGGGCGAGCAGGAGCTCATGATTCAGAAGCTGTCGGACAGC AGCAGCGGGGCGCATACGTGTAAACGGTGTTCGGACGTCATGCGTGCAAAGGTAGTTTGCT AGATGTACATAACGGTATGGGGTGTTGGCGACAGAACGAAACGGCGAGGGTGCGCAAATGTC GTGCAGAAGCGACGCTACAGCATCCATGGTACGTAGAGGCTTACTGGGTGTCAGTGCGTCGTC CGCCACTGGGGACACACTTGCAGCGAGGAGCGCCATTGTTTGGCCCACGGATTGCGTCAAGG AAAAAAA (SEQ ID NO: 1)

FIG. 6B

<u>Human</u>

>Hs_IFT20-1 chr17 gb|AC002094.1|AC002094 [expressed]
MAKDILGEAGLHFDELNKLRVLDPEVTQQTIELKEECKDFVDKIGQFQKIVGGLIELVDQ
LAKEAENEKMKAIGARNLLKSIAKQREAQQQQLQALIAEKKMQLERYRVEYEALCKVEAE
QNEFIDQFIFQK (SEQ ID NO: 23)

FIG. 6C

> Hs_IFT20-2 EST gb|AA584846.1|AA584846 QDSLGEAGLCFDELSKVRDPEVT*QTRDPKEDCMDFVGKISPFQKEIVGGLIEPVDQLAKAAENEK RKVVGAWNLLQFMAKHREAQQQQLLAQTAEEKMWLKRWWIEYE (SEQ ID NO: 24)

FIG. 6D

>Hs_IFT20-3 chr14 emb|AL121808.2|CNS01DSJ Human chromosome 14

MVKDILAEEGLHFDELNKLWVLDSEVTQQTTELKEECKNFADKTGQFQKTVGGLIELVDK
LAKKA*NAKMRAMVLR

(SEQ ID NO: 25)

Chlamydomonas

>Cr_IFT27 predicted peptide
MVKKEVKPIDITATLRCKVAVVGEATVGKSALISMFTSKGSKFLKDYAMTSG
VEVVVAPVTIPDTTVSVELFLLDTAGSDLYKEQISQYWNGVYYAILVFDVSSMESFESCK
AWFELLKSARPDRERPLRAVLVANKTDLPPQRHQVRLDMAQDWATTNTLDFFDVSANPPG
KDADAPFLSIATTFYRNYEDKVAAFQDACRNY (SEQ ID NO: 4)

FIG. 7A

FIG. 7B

(SEQ ID NO: 3)

<u>Human</u>

>Hs_IFT27 gi|12653581|gb|AAH00566.1|AAH00566 putative GTP-binding protein MVKLAAKCILAGDPAVGKTALAQIFRSDGAHFQKSYTLTTGMDLVVKTVPVPDTGDSVELFIFDS AGKELFSEMLDKLWESPNVLCLVYDVTNEESFNNCSKWLEKARSQAPGISLPGVLVGNKTDLAG RRAVDSAEARAWALGQGLECFETSVKEMENFEAPFHCLAKQFHQLYREKVEVFRALA

(SEQ ID NO: 26)

FIG. 7C

Chlamydomonas

>Cr_IFT46 predicted peptide sequence
MDDSMDYPDRDGDDLDQFQGTARSQVVQNQPHDEEVNLSESESFAGADE
PPAAPRDASLIESHDMDEGPAAPARTLSPTGYEAGKHAPGGIANSDEAPPGAYNAQEYKH
LNVGEDVRELFSYIGRYKPQTVELDTRIKPFIPDYIPAVGGIDEFIKVPRPDTKPDYLGL
KVLDEPAAKQSDPTVLTLQLRQLSKEAPGAKADMVGRLEHTDENKAKKIQQWIASINDIH
KAKPAATVNYSKRMPEIEALMQEWPPEVETFLKTMHMPSGDVELDIKTYARLVCTLLDIP
VYDDPVESLHVLFTLYLEFKNNPIFRQHMEMENKLDGMSGGGGGMMGGGADVLGL

FIG. 8A

(SEQ ID NO: 6)

>Cr IFT46 cDNA sequence ATGGATGACTCTATGGACTACCCTGACCGCGACGGGGACGACCTGGACCAGTTCCAGGGCAC AGAGCTTCGCGGGAGCGGATGAGCCTCCAGCTGCGCCTAGAGATGCGTCGCTCATAGAGTCA CACGACATGGACGAGGGCCAGCTGCTCCAGCGGGGACACTCTCACCAACGGGCTATGAGGC TGGAAAGCACGCACCTGGCGGCATCGCCAACTCGGACGAGGCACCGCCGGGTGCTTACAACG CACAGGAGTACAAGCACCTGAACGTGGGCGAGGACGTGCGCGAGCTGTTCTCCTACATCGGC CGCTACAAGCCGCAGACGGTGGAGCTGGACACGCGCATCAAGCCCTTCATCCCTGACTACATC CCCGCGGTGGGCGCATCGACGAGTTCATCAAGGTGCCGCGACCCGACACCAAGCCCGACTA CCTGGGGCTCAAGGTTCTGGACGAGCCGGCCGCCAAGCAGTCGGACCCCACGGTGCTGACGC TGCAGCTGCGGCAGCTGTCCAAGGAGGCGCCGGGCGCCAAGGCCGACATGGTGGGGCGGCTG GAGCACCGACGAGAACAAGGCCAAGAAGATCCAGCAGTGGATCGCCTCCATCAACGACAT CCACAAGCCCACCGCCACCGTCAACTACAGCAAGCGCATGCCAGAGATCGAGGCGC TGATGCAGGAGTGGCCGCGGAGGTGGAGACCTTCCTCAAGACCATGCACATGCCGTCCGGC GATGTGGAGCTGGACATCAAGACCTACGCCCGGCTGGTGTGCACGCTGCTGGACATTCCCGTG TACGACGACCCCGTGGAGAGCCTGCACGTGCTGTTCACACTGTACCTGGAGTTCAAGAACAAC CCCATCTTCAGGCAGCACATGGAGATGGAGAACAAGCTGGACGGCATGTCGGGCGGCGGCGG CGGCATGATGGGCGGCGCGCGGATGTGCTGGGCTTGTGA (SEQ ID NO: 5)

FIG. 8B

Human

>Hs_IFT46 gi[8926685]emb[CAB96537.1] hypothetical protein [Homo sapiens]
MADNSSDECEEENNKEKKKTSQLTPQRGFSENEDDDDDDDDSSETDSDSDDDDEEHGAPLEGAY
DPADYEHLPVSAEIKELFQYISRYTPQLIDLDHKLKPFIPDFIPAVGDIDAFLKVPRPDGKPDNLGLL
VLDEPSTKQSDPTVLSLWLTENSKQHNITQHMKVKSLEDAEKNPKAIDTWIESISELHRSKPPATV
HYTRPMPDIDTLMQEWSPEFEELLGKVSLPTAEIDCSLAEYIDMICA[LDIPVYKSRIQSLHLLFSLYS
EFKNSQHFKALAEGKKAFTPSSNSTSQAGDMETLTFS (SEQ ID NO.27) (

FIG. 8C

Chlamydomonas

>Cr_IFT52 predicted peptide sequence

MEEPGAEEVRILFSTAKGESHTHKAGFKQLFRRLRSTYRPDKVDKDDFTLDTLRSAHILVLGGPKE KFTAPEVDMLKKFVKNGGSILILMSEGGEEKAGTNINYFLEQFGMSVNNDAVVRTTHYKYLHPKE VLISDGILNRAVITGAGKSLNSNDDDEFRVSRGPQAFDGTGLEYVFPFGATLSVQKPAVPVLSSGKI AYPMNRPVGAVWAQPGYGRIAVLGSCAMFDDKWLDKEENSKIMDFFFKFLEPHSKIQLNDIDAEE PDVSDLKLLPDTASLADKLKGCLQEIDDVPRDWTSLFDDSLFKFDTGLIPEAVSLYEKLGVKKGQL NLIPPSFETPLPPLQPAVFPPTIREPPPPALELFDLDESFASETNRLASLTNKCHGEEDLEYYIMEAGH ILGLKLQENANAKHVLSEVFRRIAQYKMGSLGLGQTLDSMGQTLPAANQFGDQFEL

FIG. 9A

(SEQ ID NO: 8)

2 15 1 W

>Chlamvdomonas cDNA sequence

CTAATGCCATGCAGTAAGGCACTGGTATAGAAACCGTTCCCACCGCCGCGCCCAGCCCCGCGT CCTGTGAGCTGAGAGCTACTTAACAGCCATGGAGGAGCCGGGGCGCGGAGGAGGTTCGGATTC CGATTGCGTTCAACTTATCGTCCAGACAAAGTAGATAAGGATGACTTCACGCTGGACACGCTG CGGTCAGCGCACATCCTTGTOCTCGGTGGCCCGAAGGAGAAGTTCACCGCGCCTGAGGTGGA CATGCTCAAAAAGTTCGTGAAGAATGGTGGCTCCATCCTCATTCTAATGTCGGAGGGCGGCGA GGAGAAGGCGGGCACTAACATCAACTACTTCCTCGAGCAGTTTGGCATGTCGGTGAACAACG ACGCCGTGGTCCGCACCACGCACTACAAGTACCTGCACCCCAAGGAGGTGCTCATCTCGGACG GCATCCTCAACCGGGCGGTGATCACGGGCGCGGGGAAGTCGCTGAACAGCAACGACGACGAC GAGTTCCGCGTGTCGCGGGGCCGCAGGCTTTTGATGGCACGGGCCTGGAGTACGTCTTCCCC TTCGGTGCCACGCTCTCAGTGCAGAAGCCCGCGGTGCCCGTCTTGTCCAGCGGCAAAATCGCG TACCCCATGAACCGGCCAGTGGGTGCGGTATGGGCGCAGCCCGGCTACGGCCGCATCGCCGT GCTGGGCTCGTGCCCATGTTTGACGACAAGTGGCTGGACAAGGAGGAGAACTCCAAAATCA TGGACTTCTTCAAGTTCCTCGAGCCGCATTCCAAAATCCAACTCAACGACATTGACGCGG AGGAGCCGGACGTGAGCTGAAGCTGCCCGACACAGCCAGTCTGGCAGACAAGCTG AAGGGCTGCCTCCAGGAGATCGACGACGTGCCGCGGACTGGACCTCGCTGTTCGACGACTC GCTGTTCAAGTTCGACACCGGCCTCATCCCTGAGGCCGTGTCGCTGTACGAGAAGCTGGGCGT GAAGAAGGGCAGCTGAACCTCATCCCGCCCTCCTTCGAGACGCCACTGCCGCCGCTGCAGCC CGCCGTGTTCCCGCCACCATCCGTGAGCCGCCGCCGCCGGCGCTGGAGCTGTTCGACCTGGA TGAGAGCTTTGCCAGCGAGACGAACCGGCTGGCCTCGCTCACCAACAAGTGCCACGGCGAGG AGGACCTGGAGTACTACATCATGGAGGCGGCCACATCCTGGGCCTCAAGCTGCAGGAGAAC GCCAACGCCAAGCACGTGCTGTCGGAGGTGTTCCGCCGCATCGCGCAGTACAAGATGGGCAG CCTGGGCCTGGGCCAGACGCTGGACTCCATGGGCCAGACCCTGCCGGGCCCAACCAGTTCG GCGACCAGTTCGAGCTGTAAGGAGCAGCGAGCTACAGGCCGAGCAACTGCGTGGCAGGCGGC CTGGCGTGCTGGCAGCAGGATGTGCGCTTGTGCTGATGCGGTCAGCGGAGCAGCGGGCATGC TGGGCTGCTGAACAGAGCCACGCGGGAGGGTGTGCGGCGCGCCAACGGCAGCAGCATGCTGC ACGCGGGTTGTGGCCTGGCGGAAAAGCTGGGCATTCACCGGTGCCTCCTCTGAAAGGCG GCTGGGCTTGGCACCGCGTGTGCCGCTTGCGGTGTGCTGGGTGTACTGGTTTCACGCGTTCTCC AGTCTGATGAGAGGAGCCTTTATCGGATTGACAATGGTCCATGGTGAACGATGGATTATGGAT ATCGGAGTGCACAGAGGCTGACAAGATAACGTTACAGTCCAGGAGATATGTGGTGGTAGCTG CAGCAACTACAAGATGGCGTCAGTCAGACCCGACCTGTTTTGAGTGCTGCAGGCTGACACGCA TGCTGACAGAACAGACGCCGCTGCAATTGCGGTTGATATTTTAGCCAGAAGGCAATATGTGGG TGTATGCGGGGGGTGGCATGAGGCGCGCGAGTGGAGGAGTACAGGGCTGCGTCGGCCGTGCG CGTCTGCGGTTGCAACAGTGAGCTGTGTTGGGTGTGCAAGGTGGTGGGCGTGTGCATGGAGCC GTGTGGAGCAGTGTTCCCGTGGCGCTCAAGCGGCCCAGCATTCACTAAGCTCACGTGTAAAAC

(SEQ ID NO: 7)

FIG. 9B

Human

>Hs_IFT52_gi|4929575:gb|AAD34048.1:AF151811_1 CGI-53 protein [Homo sapiens]
MEKELRSTILFNAYKKEIFTTNNGYKSMQKKLRSNWKIQSLKDEITSEKLNGVKLWITAGPREKFT
AAEFEILKKYLDTGGDVLVMLGEGGESRFDTNINFLLEEYGIMVNNDAVVRNVYHKYFHPKEAL
VSSGVLNREISRAAGKAVLAIIDEESSGNNAQALTFVYPFGATLSVMKPAVAVLSTGSVCFPLNRPI
LAFYHSKNQGGKLAVLGSCHMFSDQYLDKEENSKIMDVVVFQWLTTGDIHLNQIDAEDPEISDY
MMLPYTATLSKRNRECLQESDEIPRDFTTLFDLSIFQLDTTSFHSVIEAHEQLNVKHEPLQLIQPQFE
TPLPTLQPAVFPPSFRELPPPPLELFDLDETFSSEKARLAQITNKCTEEDLEFYVRKCGDILGVTSKLP
KDQQDAKHILEHVFFQVVEFKKLNQEHDIDTSETAFQNNF (SEQ ID NO: 28)

FIG. 9C

Caenorhabditis elegans

>Ce_Osm-6 gi|2292823|emb|CAA03975.1: osm-6 [Caenorhabditis elegans]
MPPFSDEKMTNRSIGRKVLIDQSKQQQISLISGFRGVARHLKSVLTVEINTEPINLNGLEDVRMLIIP
QPKTSFGTGEIEAIWKFVEEGGSLMILSGEGGERQSLNEMIAKYGITVNKDSVIRTVFLKYFDPKEA
LVANGVINRAIAVAAKKNVSTEQKHNSQALSFIYPYGCTLDVNNRMSNVVLSSGSTSFPTSRPVAA
FHETKLNEMKKKGRVCVVGSVSMFHDTYIDKEENGKIFDTFVEFLVNGLELNTIDAAEPEINDYTN
IPDHIHMSQQIKVCMYEGELDQAISSDFMKIMDTSLHSFNLKHWPMTIRLYEALNLSPPPLTLVEPQ
FELPMPPFQPAVFPPTFQELPMPPLELFDLDEQFSSPEIQLSQLANRSEEEDLIFFIEKAGEITGISAEL
TRSERTPKKIIELAVSKLMLFKRSMMDGELEVASAFDIGEHDAHHQSFNQGEEMDEQLFSDIDEFD
DL (SEQ ID NO: 29)

FIG. 9D

Chlamydomonas

>Cr IFT57 predicted peptide sequence

MSSKRGGRSSLAKAPEEAVNGEAFAPEASPPPPGDDGDAGGEDGAPAPPPPPATKGGPVAVGRS LEIQTTPDVCMEMLADKLKLLNYEADFCRKKKPYRKPLSRLYFAVPLANSSEQFFYFTSLATWLL GLAGVELPAPKEFDDPNLTCQNILGAVKKLGFAPPSYHPTKLTVGNGKEVVGVLDGLVDFVLERR HHKYSRPAYGNDGQPEEGVQLDDEAEAAAMEGADELAMPAQNQADDDEEEEGVYVDPGRGDA AGPGTGASAAMDAEKAVLVSKVDPTLWKIELERVAPKLRITIAADSKDWRSHLDEAHQHKEVISK AWPDSKTSLERLRADLNGTLEKLQTREKFLNEQFESLMQQYRAARTTFTDVQETYNRKTEAVAD RNQEMHRIGETLEEVKAMMDEKGSNIADATPVARIKTAIKQLNKELHDMEVRIGVVSHTLLQLSL RNKRLLQAQAALSDEEED (SEQ ID NO: 10)

FIG. 10A

>Cr IFT57 cDNA sequence

GTCTTGGGAACCCAGCGAGCCGCGCTCCTTGCCACATGTCCTGCTAGCTTCTGGTTTACACCGT AGATTCATTTAAGCGAGAGACATGAGCAGCAGCGGGGTGGGCGGTCATCCTTAGCAAAGGC GCCCGAAGAGGCGTAAATGGCGAGGCATTTGCGCCTGAGGCATCTCCCCCTCCACCCGGCG GGAAATGCTGGCCGACAAGCTGAAGCTGCTAAACTACGAGGCGGATTTCTGCAGGAAGAAGA CTCCCAAGGAGTTTGATGACCCGAACTTGACGTGCCAGAACATCCTGGGTGCGGTGAAGAAG CTGGGCTTTGCGCCGCCCAGCTACCACCCTACCAAGCTCACAGTGGGCAACGCCAAGGAGGT GGTGGGTGTGCTGGACGGGCTGGTGGACTTCGTGCTGGAGCGGCGCCACCACAAGTACAGCC GGCCGCGTACGGAAATGATGGGCAACCGGAGGAGGGCGTGCAACTGGACGATGAGGCGGA GGCTGCCGCGATGGGGGTGCGGATGAGCTGGCGATGCCAGCCCAGAACCAGGCGGATGACG ATGAGGAGGAGGAGGCGTATACGTGGACCCGGGGCGCGGTGACGCCGCGGGCCCAGGGAC AGGGGCATCCGCGGCGATGGACGCGGAGAAGGCGGTGCTTGTGTCCAAGGTGGACCCCACGC TCTGGAAGATCGAGCTGGAGCGCGTGGCGCCGAAGCTGCGTATCACCATCGCCGCCGACTCG AAGGACTGGCGCTCACATCTGGATGAGGCGCACCAGCACAAGGAGGTGATCAGCAAGGCCTG GCCCGACAGCAAGACGTCGCTGGAGCGCCTGCGTGCGGACCTGAACGGCACGCTGGAGAAGC TGCAGACGCGTGAGAAGTTCCTCAACGAGCAGTTTGAGAGCCTCATGCAGCAGTACCGCGCC GCCCGCACCACGTTCACGGACGTGCAGGAGACATACAACCGCAAGACGGAGGCGGTGGCGGA CCGGAACCAGGAGATGCACCGCATCGGCGAGACGCTGGAGGAGGTGAAGGCCATGATGGAC GAGAAGGGCAGCAACATCGCGGACGCCACGCCTGTGGCTCGCATCAAGACCGCCATCAAGCA GCTTAACAAGGAGCTGCACGACATGGAGGTGCGCATCGGCGTGGTTAGCCACACGCTGCTGC AGCTATCGCTGCGCAACAAGCGATTGCTGCAGGCGCAGGCGGCTCTCAGTGACGAGGAGGAG GACTAGCTAGATCAGCGAGTGACAGAGGGCATGTGTGCGTACCGTGTGCGCGGGTACAGCCG TGGGATGGAAGAGGTGATGTGGCGGGTTGCGGACCCAGCATTCGGTAGACCAGATCACTTAT AGGTACAGAAAGACGGCTATATTGTTGGGGGGCGCGCACCCTGGCTATGTATATACAAGCCG TAGCGCAGAGCCGCTGCAAATGCGGTGCTGTGCCTGTGCTCCCGTGGGTGTGCGGCGTTCCGG TCAAGTTCATATAAGCTGTTGTGACTTGTGAGGCAGGCATGGCATATGGACAGGGCATCCCTG CAAGGAAAGCAGCAGCGGTATCCTTGTGGCGATGGGTCAAGCAGTGATGGAGGGGCGAAGC (SEQ ID NO: 9) GAGTTGCGGGCCTGTAAGCACAGGGTTGCCAAAAAAAA

Mouse

>Mm IFT57 predicted peptide sequence

MAAAAAVIPPSGLDDGVSRARGEGAGEAVVERGPGAAYHMFVVMEDLVEKLKLLRYEEELLRK SNLKPPSRHYFALPTNPGEQFYMFCTLAAWLINKTGRAFEQPQEYDDPNATISNILSELRSFGRTAD FPPSKLKSGYGEQVCYVLDCLAEEALKYIGFTWKRPSYPVEELEEETVPEDDAELTLSKVDEEFVE EETDNEENFIDLNVLKAQTYRLDTNESAKQEDILESTTDAAEWSLEVERVLPQLKVTIRTDNKDW RIHVDQMHQHKSGIESALKETKGFLDKLHNEISRTLEKIGSREKYINNQLEHLVQEYRGAQAQLSE ARERYQQGNGGVTERTRLLSEVTEELEKVKQEMEEKGSSMTDGTPLVKIKQSLTKLKQETVQMDI RIGVVEHTLLQSKLKEKCNMTRDMHAAVTPESAIGFY (SEQ ID NO: 12)

FIG. 10C

>MmIFT57 cDNA sequence

GCGAAGGCTGCAGAGATCCTGGCCGGAGCCCAGCCGGGCGCTGGGGG

TCTGAGCAGGGATGGCCGCGGGGCGGGGGTGATCCCGCCGTCGGGCTTGGACGATGGGGTG TCTCGGGCTCGCGGGAAGGCGCAGGGGAGGCTGTGGTGGAGCGCGGGCCAGGAGCGGCCTA ${\tt CCACATGTTCGTGGTGATGGAAGACTTAGTGGAGAAGCTGAAGCTGCTCCGCTACGAGGAGG}$ AGCTACTCCGAAAGAGCAATCTGAAGCCCCCGTCCAGACACTACTTTGCTCTGCCTACCAACC CAGGCGAGCAGTTCTACATGTTTTGCACTCTTGCTGCGTGGCTGATCAACAAAACTGGCCGTG CCTTTGAGCAGCCTCAAGAATACGACGATCCCAATGCAACTATATCTAATATACTCTCTGAGC TTCGCTCTTTTGGGAGAACTGCAGATTTTCCTCCTTCAAAATTAAAGTCTGGTTACGGAGAACA **AGTGTGCTATGTTCTTGATTGCTTAGCTGAAGAAGCTTTAAAATATATTGGTTTCACTTGGAAA** AGGCCATCATACCCAGTGGAAGAACTAGAAGAAGAACTGTTCCAGAAGATGATGCCGAGTT **AACATTAAGTAAAGTGGATGAAGAATTTGTGGAAGAGAGACAGATAATGAAGAAAACTTTA** TTGATCTCAACGTTTTAAAGGCCCAGACCTATCGCTTGGACACAAACGAGTCTGCCAAACAAG **AAGATATTTTGGAATCTACGACAGATGCTGCGGAATGGAGCCTAGAAGTTGAGCGTGTACTAC** CGCAGCTGAAAGTCACGATTAGGACTGACAATAAGGATTGGAGGATCCATGTTGACCAAATG CACCAGCACAAAAGTGGGATTGAATCTGCTCTGAAGGAGACCAAGGGGTTTTTGGACAAGCT CCATAATGAAATTAGCAGGACTCTGGAAAAGATTGGCAGCCGAGAAAAGTACATTAACAATC AACTTGAGCACTTGGTTCAAGAATATCGTGGGGCCCAAGCCCAGCTAAGTGAGGCAAGGGAG CGCTACCAGCAGGGCAATGGCGGAGTAACTGAACGGACCAGACTCCTCTCTGAGGTTACAGA CCTTTGGTGAAGATTAAGCAGAGCTTAACCAAGCTGAAGCAAGAAACTGTTCAGATGGACAT TAGAATCGGTGTGGTGGAGCACACGCTACTTCAGTCAAAACTCAAGGAGAAGTGCAACATGA CCAGGGACATGCATGCAGCTGTCACCCCAGAGTCAGCAATTGGCTTCTATTAAACACGTGGGC TTCCATGCTTCTGATTATTTCGTTTTTATATCAAATGATTTTTTAATGTTGCATTGATTTCCAAA CACAATTTATACTTCTTCAAGCATATTCAGTGGGTATTTTTGCACATGTGTTAATATCATGGTG ATTATGATGGCCAAAGCCTGTACAATGAATATAGTATTTAATAAAGTACTTAAAAATTAAAAAA AAAAAAAAA (SEQ ID NO: 11)

FIG. 10D

<u>Human</u>

>Hs_IFT57-1 gi|7022022|dbj|BAA91466.1| unnamed protein product [Homo sapiens]
MTAALAVVTTSGLEDGVPRSRGEGTGEVVLERGPGAAYHMFVVMEDLVEKLKLLRYEEEFLRKS
NLKAPSRHYFALPTNPGEQFYMFCTLAAWLINKAGRPFEQPQEYDDPNATISNILSELRSFGRTADF
PPSKLKSGYGEHVCYVLDCFAEEALKYIGFTWKRPIYPVEELEEESVAEDDAELTLNKVDEEFVEE
ETDNEENFIDLNVLKAQTYHLDMNETAKQEDILESTTDAAEWSLEVERVLPQLKVTIRTDNKDWR
IHVDQMHQHRSGIESALKETKGFLDKLHNEITRTLEKISSREKYINNQLENLVQEYRAAQAQLSEA
KERYQQGNGGVTERTRLLSEVMEELEKVKQEMEEKGSSMTDGAPLVKIKQSLTKLKQETVEMDI
RIGIVEHTLLQSKLKEKSNMTRNMHATVIPEPATGFY (SEQ ID NO: 30)

FIG. 10E

>Hs_IFT57-2 chromosome 12 [ESTS BF089172]
DQRIHVDQMYQHKSGIESSLKESKRFFDKLHNE
ISKTLEKISHCEKYINHQLEHRVQEYPAAQTQLSDVRSQQGSGGVIERTRLLSEATED
TEHVKLEMEEKCSSMTDGDSLVKIKQSLTKLKQETVQMDIRIGVVEHTLL (SEQ ID NO: 31)

FIG. 10F

Caenorhabditis elegans

>Ce_IFT57 gi|7504754|pir||T22994 hypothetical protein F59C6.9 - Caenorhabditis elegans MLHHIKSLKSVLSRGQEGRFGEKRHSNTTFITGIATDFTAAKLKSGAGENVIFILNSLADASLVHVG FQWQKMIPPKEEDEDTAVDEQDEDDDNDDIVEEPMNFLDDDDDDNVIEIDLKAQGLATESKNPLQ SVLQSNTDAITWKQEVERVAPQLKITLKQDAKDWRLHLEQMNSMHKNVEQKVGNVGPYLDNMS KDIAKALERIASREKSLNSQLASMMSKFRRATDTRAELREKYKAASVGVSSRTETLDRISDDIEQL KQQIEEQGAKSSDGAPLVKIKQAVSKLEEELQTMNVQIGVFEQSILNTYLRDHFNFSANLLNIM

(SEQ ID NO: 32)

FIG. 10G

16 ! (7)

Chlamydomonas

>Cr_IFT72 partial predicted peptide sequence (lacking N-terminal end)
VYVIQQEFAALKDRNEQQRKRVDEVLTERLNLESKAKQAESK
MSEIQASMDQRLNSMPPSQRNEYTTLVAEQQQLQADSKRFEEVLDELDKALQASEGELAR
NPFKQRSLQLQEQIRALTGKKYELTEEERQSKRSPEELRADLMAKIKRDNTEVEQMTQQI
RELQDQIKKMEERVKSLGGATSGAVAAEEKANREKFEELLAKERHLNNFMDGFPSRKAAK
MQEKQQKEDGIVGVLEKMVKMQGIIGSNLPSQKKYKEMQDELEYKKMQLENTQTTQERLK
EELTMRRTELEKIDTLEDKIKLELTQLAERQEAMEKEMGEFGSVEDIQRKANAARERMGA
CAVCCLKRKDLLRSIVAERGLKFQAKRAQLQDHNLQVQLEKMEAKLKNLSAGVFEMDEFI
KAKESETNYRQLASNIAALVDDLNVHVKKAVV
(SEQ ID NO: 14)

FIG. 11A

>Cr_IFT72 partial Cdna sequence (lacking 5' end) GTGTACGTGATCCAGCAGGAGTTCGCGGCGCTCAAGGACCGCAACGAGCAGCAGCGCAAGCG CGTGGACGAGGTCCACGGAGCGCCTCAACCTCGAGTCCAAGGCCAAGCAGGCCGAGTCCA ACGAATACACCACGCTCGTGGCCGAGCAGCAGCAGCTGCAGGCCGACAGCAAGCGCTTTGAG GAGGTGCTGGACGAGCTGGACAAGGCGCTGCAGGCCAGCGAGGCGAGCTGGCGCGCAACC CCTTCAAGCAGCGCAGCCTGCAGCAGAGCAGATCCGCGCGCTCACGGGGAAGAAGTAC GAGCTGACGGAGGAGGAGCGGCAGAGCAAGCGCTCGCCCGAGGAGCTGCGCGCCGACCTCAT GGCCAAGATCAAGCGAGACACCGAGGTGGAGCAGATGACGCAGCAGATCCGCGAGCTTC GGTGGCGGCGAGGAAAAGGCCAACCGCGAGAAGTTTGAGGAGCTGTTGGCCAAGGAGCGC CACCTAAACAACTTTATGGACGGCTTCCCCAGCCGCAAGGCCGCCAAGATGCAGGAGAAGCA GCAGAAGGAGGACGGCATCGTGGGCGTGCTGGAGAAGATGGTGAAGATGCAGGGCATCATTG GCTCCAACCTGCCCAGCCAGAAGAAGTACAAGGAAATGCAGGACGAGCTCGAGTACAAGAA GATGCAGCTGGAGAACACGCAGACCACGCAGGAGCGCTCAAGGAGGAGCTGACCATGCGG CGCACAGAGCTGGAGAAGATCGATACGCTGGAGGACAAGATCAAGCTGGAGCTGACGCAGCT GGCGGAGCGCAGGAGGCCATGGAGAAGGAGATGGGCGAGTTCGGCAGCGTCGAGGACATC CAGCGCAAGGCCAACGCCGCACGCGAGCGCATGGGGGCCTGCGCAGTGTGCTGTTTGAAGCG AGCTGCAGGACCACAACCTCCAGGTGCAGCTGGAGAGATGGAGGCCAAGCTGAAGAATCTG AGCGCGGGCGTATTCGAGATGGACGAGTTCATCAAGGCCAAGGAGAGCGAGACCAACTACCG CCAGCTGGCCTCCAACATAGCGGCGCTGGTAGACGACCTCAACGTGCATGTCAAGAAGGCCG TGGTGTAAGAAGGAGGCAGTGGTGTAAGGGGTCTCCGGAGGAGGGCGCGTGCCGTTGTTGGG GTGTTGGGGGCGCGCGAGAAGTACGTGCGTGTGGCGTTGTGCCTTTCAGCAGGCTGCACG TGTAGTACGGTAGTCAAGGTGAAGGGCGGCCTGGGCACAGGAGGATGCTGACGCCGTGACGG GTGACGATGACAGGCCATCGCGAGTTTGATCTCTGCTGTCGAGTCATTGACTTGGGTTCCTAG ACAGGTCGGGCTACAAGCCCGGAGGTTGATGGCTCACCTCGCAGTGCGCGGACAGCAGGTGT GGCGCATGCGCATGTGCCTCAGGAGCGCGGTGCGGACCAGGGAAGATGCGATGGGAGTAGGC TAGGCCTGTGTGAGGGCCCTTGCCGAAGCGCCACGGCCATTCCATGGCCTGGCCCGAAGGCA GCGCTCGTGGTTGGATACTGACCAGCGGCGTCAAGCGGCGTACG%TGTCAGAAGTGGAGCTA CCGCCCTGCACAAGGGGTGATGTACATACTGTTATTTAGGAGTCCGCTGCTTATAGCTACTGG + .~ GACTGCAGAAGAAGGAGGCTGCAAGGATCTGATGGAGGCGCTGGTGTGTATGGATGACGCTG (SEQ ID NO: 13) TAAGAGATGCACAAGAGAAAAAAAAAAAAAAAAA

Human

>Hs_IFT72 giil3376669!refiNP_079379.1! hypothetical protein FLJ22621 MEEVMNGYNMLKAQNDRETQSLDVIFTERQAKEKQIRSVEEEIEQEKQATDDIIKNMSLENQVKY LEMKTTNEKLLQELDTLQQQLDSQNMKKESLEAEIAHSQVKQEAVLLHEKLYELESHRDQMIAED KSIGSPMEEREKLLKQIKDDNQEIASMERQLTDTKEKINQFIEEIRQLDMDLEEHQGEMNQKYKEL KKREEHMDTFIETFEETKNQELKRKAQIEANIVALLEHCSRNINRIEQISSITNQELKMMQDDLNFK STEVQKSQSTAQNLTSDIQRLQLDLQKMELLESKMTEEQHSLKSKIKQMTTDLEIYNDLPALKSSG EEKIKKLHQERMILSTHRNAFKKIMEKQNIEYEALKTQLQENETHSQLTNLERKWQHLEQNNFAM KEFIATKSQESDYQPIKKNVTKQIAEYNKTIVDALHSTSGN (SEQ ID NO: 33)

FIG. 11C

Chlamydomonas

>Cr IFT88 predicted peptide MSYGGTEEDDLYGGYDEQSNPLAGSGGAAFKALGADGAPPGTAMMGPPGTAMKSFVPGTA MRGGTAMQQDPSLARPMTSNRGAGFTSAPNKKFDPLNRSMGSTLGSSGGGAMLVARKGDT SPEEQARGMEKTVHELLEKSAADAAKNDINSALENAMEAKKNERKLCRFREQNNMADQIN LELMYAVDFNLAHMYHMNKNYSEALNLYTAIVRNKNFPQSGWLRVNMGNIHFEQKKYPSA IKMYRMALDQISATAKEVRFKIMRNIGLSFVRMGQYPDALQSFATVMDNVPDHQTGYNLV MCNYALSDREGMKNAFIKLLKVSPSSEMDDDDDDDDDDDMQVMTMDDGLKDEMRKRNT IITRLIVKAAQLISEKVDRANGFEGGFMWCCEQLRDAGYTKLANEVELAKATRFMGQKQF DKAVGVFKDFEKKEPRVKARAATNLAFLYFLEGETDQADKYSEMALKSDRYNARAYVNKG CVLVERGDLEGARSLFNEAAGIDPYCVEAIYNLGLVSORLNELPYALAAFKKLHNMVPDN VEVIHQIATTYDMMGDFKNAVKWFELLTSLVSNDPGVLARLGAIHARFDDEAKALHYYQE SHRVYPVNMDVISWLGAYHVKSEVYEKAMPFFDLASKIQPQEVKWALMVASCYRRTNNLP AALGKYKQIHTQHPDNVECLRYLVHLCSELGRRAEAAEYMTKLKKAEKAAVPEATTAAAP AAAAAGSGMGGMGGLDDDIGSSAVSAQNRGKKMLVKEHMGGGGGKDNDDWGNEQLGDDLL PM (SEQ ID NO: 16)

FIG. 12A

3. 12

>Cr_IFT88 gi|11528334|gb|AF298884.1|AF298884 Chlamydomonas reinhardtii protein IFT88 (IFT88) CGGCAACTTGACACTTGAGCTACTCGAAGGCAGGGCCGTGTGCAGAGCTCCTTCCCCACTATC CTTCCTTTGCGTACCATACTTATCTTGCTAACAGCCTATAGAAGATGAGCTACGGGGGCCACGG AGGAGGATGACCTTTATGGAGGATATGATGAGCAATCGAACCCGCTTGCGGGCTCGGGTGGT GCCGCATTTAAGGCACTTGGGGCCGATGGAGCTCCTCCAGGCACCGCCATGATGGGGCCGCCT GGACCCCAGCCTGGCGCGCCTATGACCTCGAACCGGGGTGCTGGCTTCACGTCGGCGCCTAA CAAGAAGTTTGACCCCCTCAATCGCTCAATGGGGTCGACACTGGGCTCGTCGGGGGGGTGGCGC ACGGTGCATGAGCTGCTTGAGAAGAGCGCGGCGGACGCGGCTAAGAATGACATCAACTCGGC CCTGGAGAACGCCATGGAGGCGAAGAAGAATGAGCGAAAGCTGTGCCGCTTCCGGGAACAG AACAACATGGCGGACCAGATCAACCTGGAGCTGATGTACGCCGTGGACTTCAACCTGGCACA CATGTACCACATGAACAAGAACTACAGCGAGGCGCTGAACCTGTACACAGCCATCGTGCGCA ACAAGAACTTCCCGCAGTCGGGTTGGCTGCGCGTCAACATGGGCAACATCCACTTCGAGCAG AAGAAGTACCCCTCCGCCATCAAGATGTACCGCATGGCGTTGGACCAGATCAGCGCCACCGC CCCCGACGCCTGCAGTCCTTCGCCACGGTCATGGACAACGTGCCCGACCACCAGACCGGCTA CAACCTGGTCATGTGCAACTACGCGCTGAGCGACCGCGAGGGCATGAAGAACGCCTTCATCA AGCTGCTCAAGGTGAGCCCATCCAGCGAGATGGATGACGATGACGACGACCCCATGGGC GATGACGACATGCAAGTGATGACCATGGATGACGGGCTGAAGGACGAGATGCGCAAGCGCA ACACCATCATCACGCGCCTCATTGTCAAGGCCGCGCAGCTCATCTCCGAGAAGGTGGATCGCG CCAACGCTTTGAGGCCGCTTCATGTGGTGCTGCGAGCAGCTGCGCGACGCGGGCTACACC AAGCTGGCCAACGAGGTGGAGCTGGCCAAGGCGACCCGGTTCATGGGGCAAAAGCAGTTTGA GAGATGGCGCTCAAGAGCGACCGCTACAACGCACGAGCCTACGTCAACAAGGGATGCGTGCT GGTGGAGCGCGGCGATCTGGAGGGAGCGCGAAGCCTGTTCAACGAGGCTGCCGGCATCGACC CCTACTGCGTGGAGCCATCTACAACCTGGGCCTGGTGAGCCAGCGCCTGAACGAGCTGCCGT ACGCGCTGGCGCGTTCAAGAAGCTGCACAACATGGTGCCCGACAACGTGGAGGTCATCCAC CAGATCGCCACCACGTACGACATGATGGGCGACTTCAAGAACGCGGTCAAGTGGTTTGAGCT GCTCACCTCGCTGGTCAGCAACGACCCCGGCGTGCTGGCGCGACTGGGAGCCATCCACGCCA GGTTCGACGACGACGCCAAGGCGCTGCACTACTACCAGGAGTCGCACCGCGTGTACCCGGTG AACATGGACGTCATCTCCTGGCTGGCGCCCTACCATGTCAAATCGGAGGTGTACGAGAAGGC CATGCCCTTCTTTGACCTGGCCTCCAAGATCCAGCCGCAGGAGGTCAAGTGGGCGCTCATGGT GGCGTCCTGCTACCGCCGCACCACACCTGCCCGCCGCGCTGGGCAAGTACAAGCAAATCC ACACGCAGCACCCCGACAACGTTGAGTGCCTGCGCTACCTGGTGCACCTGTGCTCCGAGCTGG GCCGCCGCGAGGCCGCGAGTACATGACCAAGCTCAAAAAGGCGGAGAAGGCGGCGGT GCCCGAGGCAACGACAGCGGCGCGCCGCCGCGCGCAGCTGGCAGTGGCATGGGTGGCA TGGGCGGCCTGGACGACACTTGGCAGCAGCGCGGTGTCGGCGCAGAACCGCGGCAAGAAG ATGCTGGTCAAAGAGCACATGGGTGGCGGCGGTGGCAAGGACAACGACGACTGGGGAAACG AGCAGCTTGGGGACGACCTGCCCATGTAAACCGCAGTGCTGCCACAGGGCTTGGCGGGG GCGGGGCGTCAGCGAGCCAGTGGGGGCTACCGCCGCGGCCTGGCGGAGGTGGCGGCGCGCA GCTGGCGGAGCCATGCGCCCCAGGGCCAGGGGCTGTGGGGAGGTGATGGCGAGGGCGAGG ACGACGACCACCTAAAAGCGCTGGGGGCTGGGGGTTGGTGGGCGGCCGCAGCGGGGGC GCGCTGTCTGCCGGCACGGGGCGCGTGAAGGCCGATGTCAGCCGCGCCGCCTCTCACCCGGA GTTCGGGGCCGAGCCTGCGTTTGGAAAGGTGCTGAGCTTTGGCTCGGCTGGGACGTCCAGCGC ATGTGTGTGAATGTATGTGTGCTAGGTAAGCACGAGATGCGTGTGCGTTTGCTGGTTCGCG CTGCGCCACTTTTGGCTGCAGGGGTCCCCAGGTCAGTGTGAAGCCCGGCCCGGGCGGAAATG GGTGCATGGCAGTTGCGGCATGCATGCGGAAGTGAGCGAAGTGCAATAGGCTCCTGCAGG GCATGGATGCGTAGGAACAGGGCTTGAATGATATCACTATGTGGCGTTGACGGGCCCACAAC TTACATGGGAGAGGCACGCCGAAAGGGTGTGTGAGGATCAGGAGCTTGGACTTGCCGTAGTG CTGTACATGGTGCCAGTCTACGTGCGGGCATAGACACATACAGGACCTGTGCTGCTGCGGAGT CCGCATCTGCAGGAAGTCGTGCCGGGTGTCACGAGTGCGGACGATGCGGATTGTGGAGGAGT ACAGATGGGCCATCGGACATACTGGCACAGTGGCACCACCGGCCCCCTGCGACGCATGCTC GCACGACCCTGTAAAGGTCGAGCCCAAAAA

Humans

>gi|5729800|ref|NP_006522.1| Tg737 protein: Probe hTg737 (polycystic kidney disease)
MMQNVHLAPETDEDDLYSGYNDYNPIYDIEELENDAAFQQAVRTSHGRRPPITAKISSTAVTRPIA
TGYGSKTSLASSIGRPMTGAIQDGVTRPMTAVRAAGFTKAALRGSAFDPLSQSRGPASPLEAKKK
DSPEEKIKQLEKEVNELVEESCIANSCGDLKLALEKAKDAGRKERVLVRQREQVTTPENINLDLTY
SVLSNLASQYSVNEMYAEALNTYQVIVKNKMFSNAGILKMNMGNIYLKQRNYSKAIKFYRMALD
QVPSVNKQMRIKIMQNIGVTFIQAGQYSDAINSYEHIMSMAPNLKAGYNLTICYFAIGDREKMKK
AFQKLITVPLEIDEDKYISPSDDPHTNLVTEAIKNDHLRQMERERKAMAEKYITTSAKLIAPVIETSF
AAGCDWCVEVVKASQYVELANDLEINKAVTYLRQKDYNQAVEILKVLEKKDNRVKSAAATNLS
ALYYMGKDFAQASSYADIAVNSDRYNPAALTNKGNTVFANGDYEKAAEFYKEALRNDSSCTEAL
YNIGLTYEKLNRLDEALDCFLKLHAILRNSAEVLYQIANIYELMENPSQAIEWLMQVVSVIPTDPQ
VLSKLGELYDREGDKSQAFQYYYESYRYFPCNIEVIEWLGAYYIDTQFWEKAIQYFERASLIQPTQ
VKWQLMVASCFRRSGNYQKALDTYKDTHRKFPENVECLRFLVRLCTDLGLKDAQEYARKLKRL
EKMKEIREQRIKSGRDGSGGSRGKREGSASGDSGQNYSASSKGERLSARLRALPGTNEPYESSSNK
EIDASYVDPLGPQIERPKTAAKKRIDEDDFADEELGDDLLPE
(SEQ ID NO: 34)

FIG. 12C

Caenorhabditis elegans

>Ce_Osm-5 gi|12659061|gb|AAK01173.1|AF314195_1 OSM-5 [Caenorhabditis elegans]
MANSTFREDDDDFYGGFDSYDKAYDIQNITQNPQFQQAVARSSHGRRPTASQMGFRDASSSYGKP
PGTMMGNQSRMGGRTAMANNNEPARPMTAVRGAGYTSFANKVQAAERPLSTENSGENGEEKCR
QMENKVMEMLRESMLASEKKKFKEALDKAKEAGRRERAVVKHREQQGLVEMMNLDLTFTVLF
NLAQQYEANDMTNEALNTYEIIVRNKMFPNSGRLKVNIGNIHFRKREFTKALKYYRMALDQVPSI
QKDTRIKILNNIGVTFVRMGSYDDAISTFDHCVEENPNFITALNLILVAFCIQDAEKMREAFVKMIDI
PGFPDDDYMKEKDDDDVLLNQTLNSDMLKNWEKRNKSDAEKAIITAVKIISPVIAPDYAIGYEWC
LESLKQSVHAPLAIELEMTKAGELMKNGDIEGAIEVLKVFNSQDSKTASAAANNLCMLRFLQGGR
RLVDAQQYADQALSIDRYNAHAQVNQGNIAYMNGDLDKALNNYREALNNDASCVQALFNIGLT
AKAQGNLEQALEFFYKLHGILLNNVQVLVQLASIYESLEDSAQAIELYSQANSLVPNDPAILSKLA
DLYDQEGDKSQAFQCHYDSYRYFPSNLETVEWLASYYLETQFSEKSINYLEKAALMQPNVSKWQ
MMIASCLRRTGNYQRAFELYRQIHRKFPQDLDCLKFLVRIAGDLGMTEYKEYKDKLEKAEKINQL
RLQRESDSSQGKRHSANSTHSLPPSGLTGLGSGSGGSSGGGTRQYSAHVPLLLDSGTPFTVAQRDM
KAEDFSYDDPVAISSRPKTGTRKTTTDTNIDDFGDFDDSLLPD (SEQ ID NO: 35)

FIG. 12D

Chlamydomonas

>Cr_IFT122 partial predicted peptide sequence (lacking N-terminal end)
HEGHFRRAPHFAYAKETLLKMDDTKGLITLYVEAEKWDDAFLLHAHPECRQDVYLPYAKWLSN
QDRFDEARLAYQEGGFPSLATRILEQLCANAVVETRYADAAFYYYQLAMEALKSIKNPPSNMAPS
DRSALERFTELYDRAEVYYAYEVVHKSVHSPFRTTHPDTLFNASRFLLMRLLPPREVPLGVSVVN
VVYVLAKQAVEAGAFKLARFAYNKLQTLVLPAAWQAEVDLASVVIRSKPFSDKEDLLPVCWRCS
TTNPLLNTQGDYCINCGAPFIRSFVTFEHLPVVEFELEPGVDDEEAGRLLGEDAGMEAARRERKAE
RQAKAAEVGGNMLRLDQNEIDRMDDAFAAQMMVPNTTIRVDRAMLRRLKTAEVMVRTWPNPV
IPKQYFRSHGPGGAAVLQDPADTSSSRMSSRWRRWSVARRPSAAPPCAARAWRRARTPRMRVPA
ATSWAGRWAARVGPLGAPARRACPCPSSRAGRWCERGRLSGAYRVRGWIPDVGGE

(SEQ ID NO: 18)

FIG. 13A

>Cr_IFT122 partial cDNA sequence (lacking 5' end) GGCACGAGGGCCACTTCCGCCGCGCGCGCGCACTTTGCGTACGCCAAGGAGACGCTGCTCAAA ATGGACGACACCAAGGGCCTGATCACGCTGTACGTGGAGGCTGAGAAGTGGGATGACGCCTT CCTGCTGCTGCACGCGCACCCCGAGTGCCGGCAGGACGTGTACCTGCCCTACGCCAAGTGGCT CAGCAACCAGGACCGCTTCGATGAGGCGCGGCTGGCGTACCAGGAGGGCGGCTTTCCCAGCC TGGCCACCCGCATCCTGGAGCAGTTGTGCGCCAACGCGGTGGTAGAGACGCGGTACGCGGAC GCCGCCTTCTACTACTATCAGCTGGCCATGGAGGCGCTCAAGAGCATCAAGAACCCGCCCTCC AACATGGCGCCCTCGGACCGCTCCGCGCTGGAGCGCTTCACGGAGCTGTACGACCGCGCCGA GGTGTACTACGCCTACGAAGTGGTGCACAAGTCCGTGCACTCGCCCTTCCGCACCACGCACCC CCTTCAAGCTGGCGCGCTTCGCGTACAACAAGCTGCAGACGCTGGTGCTGCCGGCGGCCTGGC AGGCGGAGGTGGACCTGGCATCCGTGGTCATCCGCTCCAAGCCTTTCTCAGACAAGGAGGAC CTGCTACCGGTGTGCTGCGCGCTGCTCCACCACCACCGCTGCTCAACACGCAGGGCGACTAC TGCATCAACTGCGGCGCCCCTTCATCCGCTCCTTCGTCACCTTCGAGCACCTGCCCGTGGTGG AGTTTGAGCTGGAGCCGGGCGTGGACGACGAGGAGGCGGCCGCCTGCTGGGCGAGGACGCG GCGGCAACATGCTGCGGCTGGACCAGAACGAGATCGACCGCATGGACGACGCCTTCGCGGCC CAGATGATGGTGCCCAACACCACCATCCGCGTGGACCGGGCCATGCTGCGGCGGCTCAAGAC GGCCGAGGTCATGGTGCGCACCTGGCCCAACCCCGTCATCCCCAAGCAGTACTTCCGCAGTCA TGGACCAGGAGGTGCCGCTGCGCAGGACCCTGCGGACACTTCTTCGAGCAGGATGAGTTC GAGATGGCGGCGCTGGAGCGTGGCACGGCGCCCTTCAGCCGCACCACCGTGCGCGGCGAGGG CCTGGCGCCGGGCGAGGACGCCGAGGATGAGGGTGCCGGCGGCAACAAGCTGGGCGGCCG TTGGGCAGCGCGCGTGGGCCCATTGGGGGCGCCAGCAAGGCGCGCATGTCCGTGCCCTTCCA ATTCCGGATGTAGGCGGGAATAGGAGCTGCCGGTAGTGGCGTTGCAGCAGGCCTTCGTTAC GCAGCAGAGGGGCACGAGGAGGACGTGAACGGGTGTCTTCATGCTGCTTGTGGTCTGACTT GGTAGGACGGCGTTGGTGCCATCATTAGGCTGCCCCTGCCGGTCCACCATAGGAGCTGCGAT GGACTTGCTGGAACCAGTGTACATATGCCCGCGCAGAGACTGCGTGTCTCGAAGCGGGCACÂ **AATTGGGACATGTCGGCGTACAGACAAACGATGATGATGACAGGATGACAGTTGTTGTGCGG** CAGGGGGGCTCCCAAGCCCAGTTGAGGCCCAGGCAGGTTTGGTTGAATGGGGATGCACAGTG GCAGTGCTAATGCGCTGGCGCTATGAGCGTCCATGGTGTTGGCGGCCTCAAGTACAAGACÄCC (SEQ ID NO: 17)

<u>Human</u>

>gi|11360072'pir||T43484 hypothetical protein DKFZp434K016.1 - human (fragment) TLLQPLKGHKDTVYCVAYAKDGKRFASGSADKSVIIWTSKLEGILKYTHNDAIQCVSYNPITHQLA SCSSSDFGLWSPEQKSVSKHKSSSKIICCSWTNDGQYLALGMFNGIISIRNKNGEEKVKIERPGGSLS PIWSICWNPSSRWESFWMNRENEDAEDVIVNRYIQEIPSTLKSAVYSSQGSEAEEEEPEEEDDSPRD DNLEERNDILAVADWGQKVSFYQLSGKQIGKDRALNFDPCCISYFTKGEYILLGGSDKQVSLFTKD GVRLGTVGEQNSWVWTCQAKPDSNYVVVGCQDGTISFYQLIFSTVHGLYKDRYAYRDSMTDVIV QHLITEQKVRIKCKELVKKIAIYRNRLAIQLPEKILIYELYSEDLSDMHYRVKEKIIKKFECNLLVVC ANHIILCQEKRLQCLSFSGVKEREWQMESLIRYIKVIGGPPGREGLLVGLKNGQILKIFVDNLFAIVL LKQATAVRCLDMSASRKKLAVVDENDTCLVYDIDTKELLFQEPNANSVAWNTQCEDMLCFSGG GYLNIKASTFPVHRQKLQGFVVGYNGSKIFCLHVFSISAVEVPQSAPMYQYLDRKLFKEAYQIACL GVTDTDWRELAMEALEGLDFETAKKAFIRVQDLRYLELISSIEERKKRGETNNDLFLADVFSYQG KFHEAAKLYKRSGHENLALEMYTDLCMFEYAKDFLGSGDPKETKMLITKQADWARNIKEPKAAV EMYISAGEHVKAIEICGDHGWVDMLIDIARKLDKAEREPLLLCATYLKKLDSPGYAAETYLKMGD LKSLVQLHVETQRWDEAFALGEKHPEFKDDIYMPYAQWLAENDRFEEAQKAFHKAGRQREAVQ VLEQLTNNAVAESRFNDAAYYYWMLSMQCLDIAQDPAQKDTMLGKFYHFQRLAELYHGYHAIH RHTEDPFSVHRPETLFNISRFLLHSLPKDTPSGISKVKILFTLAKQSKALGAYRLARHAYDKLRGLYI PARFQKSIELGTLTIRAKPFHDSEELVPLCYRCSTNNPLLNNLGNVCINCRQPFIFSASSYDVLHLVE FYLEEGITDEEAISLIDLEVLRPKRDDRQLEIANNSSQILRLVETKDSIGDEDPFTAKLSFEQGGSEFV PVVVSRLVLRSMSRRDVLIKRWPPPLRWQYFRSLLPDASITMCPSCFQMFHSEDYELLVLQHGCCP (SEQ ID NO: 36) YCRRCKDDPGP

FIG. 13C

Caenorhabditis elegans

>Ce_Daf10 Z82266 F23B2.4 ${\sf MTMKKISRKLGFHGEQVCIYDLAFKPDGSELLLAADNKVYLFDVNEGGQMQTLKGHKDLVYTV}$ AWSHNGELFASGGADKLVILWNEKHEGTLRYSHTDVIQCMMFNPCNQILLTCALNEFGLWSTAD KNVIKQRSVVRCCSCAWNTDGTIFAIGHGDGTITLRKGTNATEEPSIIIQRDNEPIWGIAFSSNRTFA SRDSQGNPMGIDEIMAVIDWNKTLSFYSLDGTFIESKNLEFEPHCISYCLNGEYLLIGGSDKILKIYT RKGVLLGTVAQMDHWIWSVTVRPNSQTVAMGCVDGTIACYNLVFSTVHCVDHARYANRKSMT DVFVQNLEYRTSSNICCHDLVKKMSLYDTKLAVQLSDKIQIYKQTGGVSKNERRKQLKYTLQDTI RKDLSFSLMVVTHGHLVVCNDEKLECYDFKGIKKRSWNMKSIVRYLRVLGGPAHRETLVLGTTD GGVYKVFIDNDYPILLDSRKTAIKCIDINANRTVLASIEDTLVCKWSDIATGETLLQEPGCYSVVFN TVNENLFAFTTNNMLHVRTLAAPGHTTRGVGYVLGFVKNRTFCLVQYNLIPLEVPYTIHLYQYIER GDFKEALRIACLGVVKNDWKYLANKALDALEFDVARKAYKRVRDRKMLRMVWELKKMKSNG EPDAILRATILAYTKKFREAAKIFKENGFENRAMELFTDMRMFDDVQEVMTTASGETKKMLMRK RASWARDANQPKIAAEMLISSGDLDKAALLIIDNDWLELAIEISHKIDRSDLETMKKLSAYFIRKHE FGLASRIFQSINDMKSIVDMHVNAGHWTDAFAIADRHPKYVEDVYLPYARFLAERDRFEEAQKAF HRAGKEQEAMHVLEQLTSNSVNENRFADAGCGLNNPLLGGMSCIHCETPFIISFVSFDILPLIEFKIE NDISFDEAKELIESEPPLSDDDYNPLRGLKKGIKEIILNRESLSKLEQGHVIIQTFPPPLAPKFLFNVMP SITIAQCKGCNKVFDLDDFEMACLRKGHCPFCRTSYDRNEAFFVDEEEDEDNTNIPSFGQFSRFS

(SEQ ID NO:37)

Chlamydomonas

>Cr_IFT139 partial predicted peptide sequence (lacking C-terminal end)
MADRVLALVHYYAREGYFRHVQTVCNEVLKKRPGDGVLTFWRAYGLLMEGNTADAMRDLSSIQ
GNSDLELAVAAAQLLGHESAKVPDHDAIIDLQAKLEIEERTASDQPCLHLASFYLYTKSKERARGL
VERVLRNQPDMVPAQVLLGWIIISQQQDDEYDMLFDESELDDALSHFEQAVEHDHNDLQALLGK
AKIMELKKQLGPCLDVLTEINVRFGWFVPALVEKTRMLMMLGDWEQVTETLQRVLAADQQNIM
AQAWNCMISLTREGNNKQAAKQLQDLFSSMNRQEPKNAELFFRVARPFGRLACSDPTLLGITYLM
ADRAAQLRPEMAAYVVEAAAQKLMMDETTNATERFTQALQLDELNLEANAGALEAQIMAGELE
EAAGQIMFLEDMFTNAAAAGGGKRKGRGTGDMDDDPDMADPSLGTSSDNPTLLYLKGLLAWKQ
GMPSEGLGLLERSIAALFSAAADFHGPSLELYAALNPARITAMVRLLLQSIGGEPRAPTEAPSPLISK
VTRALDLLNKQAPALQESALLHARALYLNGNLDGALRKAGEILRMNPEESSAHLLICSVYVAQDK
PELAVSALDQAVSSNFAIRETPLYHVVQAKVLVANNKLDDAKRVLESAMNLPGVRTALTVQQRA
RLGRKVVEPTLHERATVYLLLADVLARQSKIPDAPEAKKYIQDAIREFEGTSEEVRVTVADCELAI
ARGDVEGALKKLRRIPKESPHYVKARMAMADIYLRIIRKDKAAYIKCYMDLVDHTPDYDSYCML
GEAFMQIQEPEKAVRA
(SEQ ID NO: 20)

FIG. 14A

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>Cr IFT139 partial Cdna sequence (lacking 3' end) GGGTAGTCGTAACGTCTCAAGTATCGGACGCACTATTTGCAACTGCTTATTTTCGCATGGCTCC CCCATCAATGAACTTGCTTCGTCCCTATGGCCTCCCATCGAGCGTGCAAGGTATCACCGTGTAT ACACATGCTAAATATACTTCGTTAAATTGGAGTTCACCGCGGAGGCCTGAACATTTGCCGAAC CGCTCCTGAGGAAGCAGAACGAATAGCAGTGCATACAAATAGCCATGGCGGACAGGGTACTT GCCCTGGTCCATTACTATGCTCGCGAGGGCTATTTTAGACATGTGCAGACGGTGTGCAACGAA GTGCTCAAGAAGCGGCCGGGAGATGGCGTACTCACATTCTGGCGTGCCTATGGACTGCTCATG GAGGGCAACACGGCGGACGCCATGCGTGACCTCTCCAGCATCCAGGGCAATTCTGACCTTGA GCTGGCGGTCGCAGCCGCCAACTACTGGGTCACGAATCCGCCAAGGTGCCCGACCACGATG CCATCATTGACCTCCAAGCCAAGCTGGAGATCGAGGAGCGCACCGCCAGCGACCAGCCCTGC CTGCACCTGGCCTCCTTCTACCTGTATACCAAGTCCAAGGAGCGCGCCCGCGGTCTGGTGGAG CGCGTGCTGCGCAACCAGCCCGACATGGTGCCGGCGCAGGTTCTTCTGGGCTGGATCATCATC AGCCAGCAGCAGGACGAGTACGACATGCTGTTTGACGAGTCCGAGCTGGACGACGCCCT CAGCCACTTCGAGCAGGCGGTGGAGCACGACCACAACGACCTGCAGGCGCTGCTGGGCAAAG GTGCGCTTCGGCTGGTGCCGGCGCTGGTGGAAAAGACGCGCATGCTCATGATGCTGGGC GACTGGGAGCAGGTGACGGAGACGCTGCAGCGGGTGCTTGCGGCGGACCAACAGAACATCAT GGCGCAGGCCTGGAACTGCATGATCTCCCTCACTCGCGAGGGCAACAACAAGCAGGCGGCCA AGCAGCTGCAGGACCTGTTCAGCTCAATGAACCGCCAGGAGCCCAAGAACGCCGAGCTCTTC TTCCGCGTCGCCCGCCCTTCGGCCGCCTGCCCGCCCACGCTGCTGGGCATCACC TACCTCATGGCCGACCGCGCGCGCAGCTCAGGCCGGAGATGGCGGCCTACGTGGTGGAGGC AGCTGCTCAGAAGCTGATGATGGACGAGACCACCAACGCCACGGAGCGCTTCACGCAGGCGC TACAGCTGGACGAGCTGAACCTGGAGGCCAACGCGGGCGCGCTGGAGGCGCAGATCATGGCG GGCGAGCTGGAGGAGGCGGCGGGGCAGATCATGTTCCTGGAGGACATGTTCACCAACGCCGC GGCGGCTGGCGGCGAAGCGCAAGGGCCGCGCGCACCGGCGACATGGACGACCCCGAT ATGGCCGACCCCAGTCTGGGCACCTCCTCCGACAACCCCACGCTGCTCTACCTCAAGGGTCTG CTGGCCTGGAAGCAGGGCATGCCGTCCGAGGGCCTGGGTCTGCTGGAGCGCTCCATTGCCGCC CTGTTCTCCGCCGCCGACTTCCACGGCCCCAGCCTGGAGCTGTACGCGGCGCTCAACCCG GCGCGCATCACCGCAATGGTGCGGCTGCTGCTGCAGAGCATCGGCGGTGAGCCGCGCGCTCC CACTGAGGCGCCGTCTCCGCTCATCAGCAAGGTCACCCGCGCGCTGGACCTGCTGAACAAGCA TGGACGCCCCCCAAGGCGGCGAGATCCTGCGCATGAACCCCGAGGAGAGCTCCGCG CACCTGCTCATCTGTTCCGTGTACGTGGCGCAGGACAAGCCCGAGCTGGCCGTCAGCGCGCTG GACCAGGCCGTCAGCAGCAACTTCGCGATCCGCGAGACGCCTCTGTACCACGTGGTCCAGGCC AAGGTGCTGGTGGCCAACAACAAGCTGGACGACGCCAAGCGCGTCCTGGAGTCCGCCATGAA TCGAGCCCACGCTGCACGAGCGCCCACCGTGTACCTGCTGCTGGCGGACGTGCTGGCGAGG CAGTCCAAGATACCGGACGCACCAGAGGCCAAGAAGTACATCCAAGACGCCATCCGCGAGTT CGAGGGCACCAGCGAGGAGGTGCGCGTCACGGTGGCGACTGCGAGCTGGCCATTGCGCGCG GCGACGTGGAGGGCGCGCTCAAGAAGCTGCGGCGCATCCCCAAGGAGTCTCCGCACTACGTG AAGGCGCGCATGGCCATGGCCGACATCTACCTGCGCCACCGCAAGGACAAGGCCGCCTACAT CAAGTGCTACATGGACCTGGTGGACCACACGCCCGACTACGACAGCTACTGCATGCTGGGCG (SEQ ID NO: 19) AGGCGTTCATGCAGATCCAGGAGCCGGAGAAGGCAGTGCGCGCT

FIG. 14B

<u>Human</u>

>Hs IFT139-1 refiNT 005498.3 Hs3 5655 Homo sapiens chromosome 3 SFIQAGIIYYSQEKYFHHVQAAAVGLEKFSNDPVLKFFKAYGVLKEDREAIQELEYSLKEIRKTVSG TALYYAGLFLWLIGRHDKAKEYIDRMLKISRGFREAYVLRGWVDLTSDKPHTAKKAIEYLEQGIQ DTKDVLGLMGKAMYFMMQQNYSEALEVVNQITVTSGSFLPALVLKMQLFLARQDWEQTVEMG HRRILEKDESNIDACQILTVHELAREGNMTTQATNHVRNLIKALETREPENPSLHLKKIIVVSRLVC GSHQVILGLVCSFIERTFMATPSYVHVATELGYLFILKNQVKEALLWYSEAMKLDKDGMAGLTGII LCHILEGHLEEAEYRLEFLKEVQKSLGKSEVRAPWGYGLLQDDVLCCPPTPTFQCKVAWTFTLPLP TKSAQADIGTETRSSLPQVLIFLQALLMSRKHKGEEETTALLKEAVELHFSSMQGIPLGSEYFEKLD PYFLVCIAKEYLLFCPKQPRLPGQIVSPLLKQVAVILNPVVKAAPALIDPLYLMAQVRYYSGELEN AQSILQRCLELDPASVDAHLLMCQIYLAQGNFGMCFHCLELGVSHNFQVVRDHPLYHLIKARALN KAGDYPEAIKTLKMVIKLPALKKEEGRKFLRPSVQPSQRASILLELVEALRLNGELHEATKVMQDT INEFGGTPEENRITIANVDLVLSKGNVDVALNMLRNILPKQSCYMEAREKMANIYLQTLRDRRLYI RCYELCEHLPGPHTSLLLGDALMSILEVSERPHSLAKWPPSLPSPVGEKRKTQRHFPHQPEKALEV YDEAYRQNPHDASLASRIGHAYVKAHQYTKAIEYYEAAQKINGQDFLCCDLGKLLLKLKKVNKA EKVLKQALEHDIGVQDIPSMMNDVKCLLLLAKVYKSHKKEAVIETLNKVIDRWTQALALDLQSRI LKRVPLEQPEMIPSQKQLAASICIQFAEHYLAEKEYDKAVQSYKDVFSYLPTDNKVLMADLMFRK QKHEAAINLYHQVLEKAPGDNFLVLHKLIDLLRRSGKLEDIPAFFELAKKVSSRVPLEPGFNYCRGI YCWHIGQPNEALKFLNKARKDSTWGQSAIYHMVQICLNPDNEVVGGEAFENLIPRSNTCSYMEKK ELEQQGVSTAEKLLREFYPHSDSSQTQLRLLQGLCRLATREKANMEAALGSFIQIAQAEKDSVPAL LALAQAYVFLKQIPKARMQLKRLAKTPWVLSEAEDLEKSWLLLADIYCQGSKFDLALELLRRCVQ YNKAQSCYKAYEYMGFIMEKEQSYKDAVTNYKLAWKYSHHANPAIGKATSQGARETWEGGGQ EPHHDPRTQGLYPGCYENQRGSQVTRVPPSLLSMSPVGFKLAFNYLKDKKFVEAIEICNDVSQQP (SEQ ID NO: 38) WWGGPGVVVGNPA

FIG. 14C

>Hs IFT139-2 refiNT 005239.3|Hs2 5396 Homo sapiens chromosome 2 INYYCQERYFHHVLLVASEGIKRYGSDPVFRFYHAYGTLMEGKTQEALREFEAIKNKQDVSLCSLL ALIYAHKDREAILESDARVKEQRKGAGEKALYHAGLFLWHIGRHDKAREYIDRMIKISDGSKQGH VLKAWLDITRGKEPYTKKALKYFEEGLQDGNDTFALLGKVSWRQNYSGALETVNQIIVNFPSFLP AFVKKMKLQLALQDWDQTVETAQRLSNKIIFFSFCGRSQLILQKIQTLLERAFSLNPQQSEFATELG YQMILQGRVKEALKWYKTAM TLDETSVSALVGFIQCQLIEGQLQDADQQLEFLNEIQQSIGKSAV LIYLHAVLAMKKNKRQEEVINLLNDVLDTHFSQLEGLPLGIQYFEKLNPDFLLEIVMEYLSFCPMQ VSNYGFLLGDIEAAFNNLQHCLEHNPSYADAHLLLAQVYLSQEKVKLCSQSLELCLSYDFKVQVR DYPLYHLIKAQSQKKMGEIADAIKTLHMAMSLPGMKRIGASTKSKDRKTEVDTSHRLSIFLELIDV HRLNGEHEATKVLQDAIHEFSGTSEEVRVTIANADLALAQGDIERALSILQNVTAEQPYFIEAREK MADIYLKHRKDKMLYITCFAITYYEAALKTGQKNYLCYDLAELLLKLKWYDKAEKVLQHALAH EPGMKARELQARVLKRVQMEQPDAVPAQKHLAAEICAEIAKHSVAQRDYEKAIKFYREALVHCE TDNKVDNYMTLSRLIDLLRRCGKLEDVPRFFSMAEKRNSRAKLEPGFQYCKGLYLWYTGEPNDA LRHFNKARKDRDWGQNALYNMIEICLNPDNETVGGEVFENLDGDSNSTEKQESVQLAVRTAEKL LKELKPQTVQGHVQLRIMENYCLMATKQKSNVEQALNTFTEIAASEKEHIPALLGMATAYMILKQ TPRARNQLKRIAKMNWNAIDAEEFEKSWLLLADIYIQSAKYDMAEDLLKRCLRHNRSCCKAYEY (SEQ ID NO: 39) MGYIMEKEQAYTDAALNYEMAWKYSNRTNPAVG

FIG. 14D

Caenorhabditis elegans

>gi|7511091|pir||T29012 hypothetical protein ZK328.7 - Caenorhabditis elegans MKVAANELAISTIHFLPGHIEKAKASIMMKDWRGVMDCIMNADQPEGSNPYIEVLRTVHGICYAG EVSMLKRTLQLLLKSLDENEATNHVLYARITKLLVSISGRDEKILRHARDFLTRALKISRKPDYVAL ${\bf SMRIAFGLGGAKEVSTLSQELVALDCEDSYAVLSSVVSMLMISRVSDARAQFDILPSAHPKLLESPL}$ YYLIASVLAKQSKDKSFENFRQHIENLVEMLRNQLQSFPFGLDYLSLFSSDLLYSAVEQCFDFYPLV PIKAPDDCMKLTAKTLQMIYDVAPGLAHCTLQLARNSYLCSNTNAAEKWIEKVLDKDDSLADAHI LRAELILDRGGKITDADDALVTGLNFNFKLRETSLYHLIKSKTFKKRNENDEAIKTLKMALQIPRKE PSKNLFQPKESADTHKISVQLELIDTLQHMKRIQEAETTMTDALAEWAGQPEQDQLVIAQAQLYL TKGHVERALGILKKIQPGQSNFHLSRIKMAEIYLEEKKDKRMFAACYRELLKVEATPGSYSLLGDA FMKVQEPEDAINFYEQALKMQSKDVQLAEKIGEAYVMAHLYSKAVNFYESSMNIYKDKNMRLK LANLLLKLRNFEKCEKVLRAPFERDPEPVGTETIQTYIQFLLLLAECHEMMDNVPEAMNDFEKAKS LHSRIQDKTLTAALKKEGARICNLQAELLYRRREFSQAVDICKQALAYHETDLKANLLLSKIFKEE NKWTLVLQPCQTVIQVDPHNDEANSILADFYYIRSEAAHASTSYTTLLNTNPQHWHALSRVVELF CRNGEQNAAEKHLDRAKEVNPRCVTESGYNVCRGRFEWYTGDQNEALRYYSRTKDSAAGWREK ALYYMIDICLNPDNEIIIDENSVENPETTKIIYLVSELWKKLVNSKNLPNITSIYSENFQSTDRFLLAQ NFIRMHTTDKSAIQAALDEFNRMAFNADRSQVTNVGAVFGVARGHVLLKQVQKAKTVLKMVNG RVWNFDDSDYLEKCWLMLADIYINQNKNDQAVTFLDLVFKYNCNCLKAFELYGYMREKEQKYV EAYKMYEKAFMATKERNPGFGYKLAFTYLKAKRLFACIETCQKVLDLNPQYPKIKKEIMDKAKA (SEO ID NO: 40)

FIG. 14E

Che-2

Chlamydomonas

>Cr_Che-2 predicted peptide sequence
MRLKVKQSSANVHSELTAAVGWNVWNELFTCSDDQTIHKWNMLGEPEQKVSTLDAYFTDMHW
YPVSSKKTQAGGTDVFAVACTDGSVKILSRTGRVEKSIEGHKGACISLRWSYDGTALATAGEDGS
VKIWSRNGMLRSTLAQADSPVYSIVWAYDCDQLCYCTGSNVVIKSLSSNAKQNAWKAHDGVVL
KVDWSPINHLIITGGEDCKYKVWDSFGRLLFQSGLFDYPVTSVAWAPSGELFAVGGFNTLQLCDR
MGWAYSKIHLNDTGSIMTLSWTADSTQLAGGGGSGGVVFGQVVDLALEDGKMQVTVVDDMRIV
VNDILNENADELPEFRDRVIKVSLGYGYLIVATATQCHVYNTTNLGTPHIFDLKDTVTLLLQAERH
FLLLDNSAGIQIYTYEGRQICNPRFQGLRTELLNAQMITLSNDTIAVLDQQASGTTVRFFDTAQGRP
VGEPWQHTLEVKEIALSQAGTINDRQLIVIDRNRDLYLLPVMKRHVAKLAAMCDSARWHDSTAM
LSAMVDQRLCVWYYPSEVYVDKDLLAKTRYTKSDSDFGKSAQIQLFAGNRCLVRRSDGVLVSAA
TSPYPAVLYDMIRKQQWDKATRLCRFIKDPTMWATLAAMAMAAKELNTAEVAFAAIDEVDKTH
FVRKVKQIPTEEGRNAELAVYRRKPEEGESILLQAGLVFRAIKLNIKLFNWERALXLATQHKQHQD
TVLWYRQQFLKNAKLAESITRFMQMNESVVVDQAAVKKKIEEERIKESQRPGAKRYV

(SEQ ID NO: 22)

FIG. 15A

E. 31/

>Cr Che-2 cDNA sequence

ATGCGTCTCAAGGTCAAGCAGTCCAGCGCGAATGTGCACAGCGAATTAACAGCAGCTGTGGG CTGGAATGTCTGGAATGAACTGTTCACTTGTAGCGACGACCAGACTATTCACAAATGGAACAT GCTGGGGGAGCCAGAGCAGAAGGTCAGCACTCTGGACGCATACTTCACGGATATGCACTGGT GACGGCTCTGTAAAAATCCTCAGCCGCACGGGCCGCGTGGAGAAGTCCATTGAGGGGCACAA ACGGGTCGGTAAAGATCTGGTCGCGCAACGGCATGCTGCGCTCCACGCTAGCGCAGGCGGAC AGCCCCGTGTACTCGATTGTGTGGGCCTACGACTGCGACCAGCTGTGCTACTGCACCGGCTCC AACGTGGTCATCAAGTCGCTGTCCTCCAACGCCAAGCAGAACGCGTGGAAGGCGCACGACGG CGTGGTGCTCAAGGTGGACTCGAGCCCCATCAACCACCTCATCACAGGCGGCGAGGACT GCAAGTACAAGGTGTGGGACAGCTTTGGGCGGCTGTTCCAGAGCGGGCTGTTCGACTACC CGGTCACGTCGGTGGCGTGGGCGCCCAGCGGCGAGCTGTTCGCGGTGGGCGGCTTCAACACG CTGCAGCTGTGACCGCATGGGCTGGGCCTACTCCAAGATCCACCTCAACGACACGGGCAGC CGTGGTGTTCGGCCAGGTGGTGGACCTGGCGCTGGAGGACGGCAAGATGCAGGTGACGGTGG TGGACGACATGCGCATTGTGGTGAACGACATCTTGAACGAGAACGCGGACGAGCTGCCCGAG TTCCGTGACCGCGTCATCAAGGTGTCGCTAGGGTACGGCTACCTGATCGTGGCCACCGCGACG CAGTGCCACGTGTACAACACCACCAACCTGGGCACGCCGCACATCTTTGACCTCAAAGACACG GTCACCCTGCTGCAGGCTGAGCGGCACTTCCTGCTGCTGGACAACTCGGCGGGCATCCAG ATCTACACCTACGAGGGCCGCCAGATCTGCAACCCGCGCTTCCAGGGCCTGCGCACCGAGCTG CTGAACGCGCAGATGATCACGCTGTCCAACGACACGATAGCGGTGCTGGACCAGCAGGCCAG ACACGTTGGAGGTGAAGGAGATCGCGCTGAGCCAGGCCGGCACCATCAACGACCGCCAGCTC ATCGTCATCGACCGCAACCGCGACCTGTACCTGCCCGTCATGAAGCGCCACGTGGCCAAG CTGGCGGCCATGTGCGACTCGGCGCGCTGGCACGACACCGCCATGCTGTCCGCCATGGTG GACCAGCGCCTGTGTGTGTGTGTACTACCCCAGCGAGGTGTACGTGGACAAGGACCTGCTGGCC AAGACGCGCTACACCAAGTCCGACTCGGACTTTGGCAAGTCGGCCCAGATCCAGCTCTTCGCC GGCAACCGCTGCCTGGTGCGCCGCTCCGACGGCGTGCTGGTCTCCGCCGCCACCTCGCCCTAC CCTGCCGTACTGTACGACATGATCCGCAAGCAGCAGTGGGACAAGGCCACGCGGCTGTGTCG CTTCATCAAGGACCCCACCATGTGGGCCACGCTGGCGGCGATGGCCATGGCGGCTAAGGAGC TGAACACGGCGGAGGTGGCGTTCGCGGCGATTGACGAGGTGGACAAAACGCACTTTGTGCGC AAGGTGAAGCAGATCCCCACGGAGGAGGGCCGCAACGCCGAGCTGGCGGTGTACCGGCGCA AGCCCGAGGAGGCGAGTCCATACTGCTGCAGGCCGGCCTGGTCTTCCGCGCCATCAAGCTG AACATCAAGCTGTTCAACTGGGAGCGCGCGCTGSACCTGGCCACGCAGCACAAGCAGCACCA GGACACGGTGCTGTGGTACCGCCAGCAGTTCCTCAAGAACGCCAAGCTCGCCGAGTCCATCAC GCGCTTCATGCAGATGAACGAGTCGGTGGTTGTGGACCAGGCGGCGGTGAAGAAGAAGATCG AGGAGGAGCGCATCAAGGAGTCGCAGCGGCCAGGCGCCAAGCGCTACGTGTAA

(SEQ ID NO: 21)

FIG. 15B

Human

>Hs_Che-2 gi|7243129|dbj|BAA92612.1| KIAA1374 protein [Homo sapiens]
IELVSCVGWTTAEELYSCSDDHQIVKWNLLTSETTQIVKLPDDIYPIDFHWFPKSLGVKKQTQAESF
VLTSSDGKFHLISKLGRVEKSVEAHCGAVLAGRWNYEGTALVTVGEDGQIKIWSKTGMLRSTLA
QQGTPVYSVAWGPDSEKVLYTAGKQLIIKPLQPNAKVLQWKAHDGIILKVDWNSVNDLILSAGED
CKYKVWDSYGRPLYNSQPHEHPITSVAWAPDGELFAVGSFHTLRLCDKTGWSYALEKPNTGSIFN
IAWSIDGTQIAGACGNGHVVFAHVVEQHWEWKNFQVTLTKRRAMQVRNVLNDAVDLLEFRDRV
IKASLNYAHLVVSTSLQCYVFSTKNWNTPIIFDLKEGTVSLILQAERHFLLVDGSSIYLYSYEGRFIS
SPKFPGMRTDILNAQTVSLSNDTIAIRDKADEKIIFLFEASTGKPLGDGKFLSHKNEILEIALDQKGL
TNDRKIAFIDKNRDLCITSVKRFGKEEQIIKLGTMVHTLAWNDTCNILCGLQDTRFIVWYYPNTVY
VDRDILPKTLYERDASEFSKNPHIVSFVGNQVTIRRADGSLVHISITPYPAILHEYVSSSKWEDAVRL
CRFVKEQTMWACLAAMAVANRDMTTAEIAYAAIGEIDKVQYINSIKNLPSKESKMAHILLFSGNI
QEAEIVLLQAGLVYQAIQININLYNWERALELAVKYKTHVDTVLAYRQKFLETFGKQETNKRYLH
YAEGLQIDWEKIKAKIEMEITKEREQSSSSQSSKSIGLKP
(SEQ ID NO: 41)

FIG. 15C

Caenorhabiditis elegans

>Ce_Che-2 gi|4468141|emb|CAB38019.1| CHE-2 protein [Caenorhabditis elegans]
MKLKLSASRKTRHTEMVCGVGWIGTEAILSAADDHVFLLTNTATNESQQILNMPETFFTSLHIFP
RSQTKGGQNDVFAVSTSDGKINILSRNGKVENMVDAHNGAALCARWNSDGTGLLSSGEDGFVK
MWSRSGMLRSVLAQFATAVYCVAWDSTSSNVLYCNADHCYIKSLKMQVAPIKWKAHDGIILCCD
WNPTSDLIVTGGEDLKFKVWDGFGQILFNSSVHDYPITSISWNTDGTLFAVGSHNILRLCDKSGWS
HSLEKMNAGSVMALSWSPDGTQLAVGTAAGLVFHAHIIDKRLTYEEFEIVQTQKTVIEVRDVSSE
VSRETLETKERISKIAILYKYLIVVTSSHIYIYSSKNWNTPTMIEYNERTVNIIVQCEKIFLVSDGMTIT
IFTYEGRKLINLNPPGQVMALLDERKIDLANDTLVVRDRADNKVLHFFDPTTGKAQGDGNLKHEH
DIVELTVNQCGPLNDRNVAFRDQIGAVHIAMVKTFGVSQRMVKIGSLVEQLVFNDVTNMLCGISE
GKIAVWPLPNVAFHDRNLLQKSLIQKNIGSVGKFPQLANFAGNTIVIRKSDGCLLPTGILPFYGTLIT
MASQSKWDQAIRLCRSIGNDTMWATFAGLAVLHKNMIVMEIAYAALEDDEKVSLINEIKDKTDK
ETRQAMQVVLTGKLADADVLLERSGLSFRSLMLNIQMFKWKRALELGLKNKQWLEIVMGYREK
YLKNCGQKETDPLFLKHMSEVEIDWVHIRELIAAEKAKGNN
(SEQ ID NO: 42)

FIG. 15D

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